Primary structure of human nonmuscle-type cofilin (AC: P23528)

MASGVAVSDG VIKVFNDMKV RKSSTPEEVK KRKKAVLFCL SEDKKNIILE EGKEILVGDV
GQTVDDPYAT FVKMLPDKDC RYALYDATYE TKESKKEDLV FIFWAPESAP LKSKMIYASS
KDAIKKKLTG IKHELQANCY EEVKDRCTLA EKLGGSAVIS LEGKPL

The underlined portions are the sites analyzed for sequence by MS and MS/MS.

Met Ala Ser Gly Val Ala Val Ser Asp Gly Val Ile Lys Val Phe Asn
5 10 15
Asp Met Lys Val Arg Lys Ser Ser Thr Pro Glu Glu Val Lys Lys Arg
20 25 30
Lys Lys Ala Val Leu Phe Cys Leu Ser Glu Asp Lys Lys Asn Ile Ile
35 40 45
Leu Glu Glu Gly Lys Glu Ile Leu Val Gly Asp Val Gly Gln Thr Val
50 55 60
Asp Asp Pro Tyr Ala Thr Phe Val Lys Met Leu Pro Asp Lys Asp Cys
65 70 75 80
Arg Tyr Ala Leu Tyr Asp Ala Thr Tyr Glu Thr Lys Glu Ser Lys Lys
85 90 95
Glu Asp Leu Val Phe Ile Phe Trp Ala Pro Glu Ser Ala Pro Leu Lys
100 105 110
Ser Lys Met Ile Tyr Ala Ser Ser Lys Asp Ala Ile Lys Lys Lys Leu
115 120 125
Thr Gly Ile Lys His Glu Leu Gln Ala Asn Cys Tyr Glu Glu Val Lys
130 135 140
Asp Arg Cys Thr Leu Ala Glu Lys Leu Gly Gly Ser Ala Val Ile Ser
145 150 155 160
Leu Glu Gly Lys Pro Leu SEQ ID NO: 1
165

Fig. 1

cDNA of human placentaL nonmuscle-type cofilin

(AC: D00682)

atggcctccg gtgtggctgt ctctgatggt gtcatcaagg tgttcaacga catgaaggtg 60

cgtaagtctt caacgccaga ggaggtgaag aagcgcaaga aggcggtgct cttctgcctg 120

agtgaggaca agaagaacat catcctggag gagggcaagg agatcctggt gggcgatgtg 180

ggccagactg tcgacgatcc ctacgccacc tttgtcaaga tgctgccaga taaggactgc 240

cgctatgccc tctatgatgc aacctatgag accaaggaga gcaagaagga ggatctggtg 300

tttatcttct gggccccccga gtctgcgccc cttaagagca aaatgattta tgccagctcc 360

aaggacgcca tcaagaagaa gctgacaggg atcaagcatg aattgcaagc aaactgctac 420

gaggaggtca aggaccgctg caccctggca gagaagctgg ggggcagtgc ggtcatctcc 480

ctggagggca agcctttgtg a SEQ ID NO: 2 501

The underlined portions are the sites where two oligomers were synthesized as primers.

Fig. 2

Alignment of the base sequences for nonmuscle-type cofilin derived from human placenta (upper) and from human S6 cells (lower).

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                    10        20        30        40        50
Placental cDNA    1 ATGGCCTCCG GTGTGGCTGT CTCTGATGGT GTCATCAAGG
TGTTCAACGA  50
S6 cDNA                 1 ATGGCCTCCG GTGTGGCTGT CTCTGATGGT GTCATCAAGG
TGTTCAACGA  50

                    60        70        80        90       100
Placental cDNA   51 CATGAAGGTG CGTAAGTCTT CAACGCCAGA GGAGGTGAAG
AAGCGCAAGA  100
S6 cDNA                 51 CATGAAGGTG CGTAAGTCTT CAACGCCAGA
GGAGGTGAAG AAGCGCAAGA  100

                   110       120       130       140       150
Placental cDNA  101 AGGCGGTGCT CTTCTGCCTG AGTGAGGACA AGAAGAACAT
CATCCTGGAG  150
S6 cDNA                 101 AGGCGGTGCT CTTCTGCCTG AGTGAGGACA
AGAAGAACAT CATCCTGGAG  150

                   160       170       180       190       200
Placental cDNA  151 GAGGGCAAGG AGATCCTGGT GGGCGATGTG GGCCAGACTG
TCGACGATCC  200
S6 cDNA                 151 GAGGGCAAGG AGATCCTGGT GGGCGATGTG
GGCCAGACTG TCGACGACCC  200

                   210       220       230       240       250
Placental cDNA  201 CTACGCCACC TTTGTCAAGA TGCTGCCAGA TAAGGACTGC
CGCTATGCCC  250
S6 cDNA                 201 CTACGCCACC TTTGTCAAGA TGCTGCCAGA TAAGGACTGC
CGCTATGCCC  250

                   260       270       280       290       300
Placental cDNA  251 TCTATGATGC AACCTATGAG ACCAAGGAGA GCAAGAAGGA
GGATCTGGTG  300
S6 cDNA                 251 TCTATGATGC AACCTATGAG ACCAAGGAGA
GCAAGAAGGA GGATCTGGTG  300

                   310       320       330       340       350
Placental cDNA  301 TTTATCTTCT GGGCCCCCGA GTCTGCGCCC CTTAAGAGCA
AAATGATTTA  350
S6 cDNA                 301 TTTATCTTCT GGGCCCCCGA GTCTGCGCCC CTTAAGAGCA
AAATGATTTA  350

                   360       370       380       390       400
Placental cDNA  351 TGCCAGCTCC AAGGACGCCA TCAAGAAGAA GCTGACAGGG
ATCAAGCATG  400
S6 cDNA                 351 TGCCAGCTCC AAGGACGCCA TCAAGAAGAA
GCTGACAGGG ATCAAGCATG  400

                   410       420       430       440       450
Placental cDNA  401 AATTGCAAGC AAACTGCTAC GAGGAGGTCA AGGACCGCTG
CACCCTGGCA  450
S6 cDNA                 401 AATTGCAAGC AAACTGCTAC GAGGAGGTCA
AGGACCGCTG CACCCTGGCA  450

                   460       470       480       490       500
Placental cDNA  451 GAGAAGCTGG GGGGCAGTGC GGTCATCTCC CTGGAGGGCA
AGCCTTTGTG  500
S6 cDNA                 451 GAGAAGCTGG GGGGCAGTGC GGTCATCTCC
CTGGAGGGCA AGCCTTTGTG  500

                   510       520       530       540       550
Placental cDNA  501 A..... ..... ..... ..... ..... 550
S6 cDNA                 501 A..... ..... ..... ..... ..... 550
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SEQ ID NO: 2
SEQ ID NO: 8

The two bases that differ between the two sequences are marked by shadowing and are both due to silent mutation.

Fig. 3